

SEQUENCE LISTING

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KOBAYASHI, TAKEHIKO

<120> METHOD FOR AMPLIFYING FOREIGN GENES

<130> 084335/0135

<140> 09/807,409

<141> 2001-04-13

<150> JP 10/292697

<151> 1998-10-15

<150> PCT/JP99/05673

<151> 1999-10-14

<160> 28

<170> PatentIn Ver. 2.1

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400>1

gcgtcgacgt tgcggccata tctaccag

28

<210> 2

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400>2

ccagcctcgc atatgaccaa taccagctta actacagttg

40

<210> 3

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400>3

ttcctgatat gcgaggctgg agagcctgac cgagtagtgt

40

<210> 4
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic DNA

<400>4
 gcgtcgacag attgcagcac ctgagttt 28

<210> 5
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic DNA

<400>5
 gcgtcgacgt tgcggccata tctaccag 28

<210> 6
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic DNA

<400>6
 ccagcctcgc atatgaccaa taccagctta actacagttg 40

<210> 7
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic DNA

<400>7
 ccatcagata tcgttcggtc aatccatgcc ataacaggaa 40

<210> 8
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic DNA

<400>8
gggagctctg aatagacata ggagtaag 28

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 9
ggggtaccat aaggagatca gtgcgctg 28

<210> 10
<211> 40
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400>10
ccagcctcgc atatgaccaa taccagctta actacagttg 40

<210> 11
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400>11
tggctacgtc ctgatgcagg gcaactaatt ttcgtcaaga 40

<210> 12
<211> 28
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400>12
ggggtacctg gattgttttc agcctctg 28

<210> 13
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<223> Description of Artificial Sequence: Synthetic DNA

<400> 13

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<210> 14

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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tgatttgatca aacgcctgcc accaataggt gatgaaactg 40

<210> 15

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400>15

ggcaggcggtt tgacaaatca tctggagata tgattaaccc 40

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

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<210> 17

<211> 20

<212> DNA

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<223> Description of Artificial Sequence: Synthetic DNA

<400>17

gttgcgcca tatctaccag 20

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400>18

agattgcagc acctgagttt

20

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400>19

gttgcgcca tatctaccag

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<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400>20

tgaatagaca taggagtaag

20

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 21

ataaggagat cagtgcgctg

20

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic DNA

<400>22

tggattgttt tcagcctctg

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<210> 23
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic DNA

<400> 23
 cgtagacgtg aggaagatga 20

<210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic DNA

<400>24
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<210> 25
 <211> 566
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 25
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 1 5 10 15
 Val Pro Ser Glu Ser Val Thr Arg Lys Ser Gln Arg Arg Lys Ala Thr
 20 25 30
 Ser Pro Gly Glu Ser Arg Glu Ser Ser Lys Asp Arg Leu Leu Ile Leu
 35 40 45
 Pro Ser Met Gly Glu Ser Tyr Thr Glu Tyr Val Asp Ser Tyr Leu Asn
 50 55 60
 Leu Glu Leu Leu Glu Arg Gly Glu Arg Glu Thr Pro Ile Phe Leu Glu
 65 70 75 80
 Ser Leu Thr Arg Gln Leu Thr Gln Lys Ile Tyr Glu Leu Ile Lys Thr
 85 90 95
 Lys Ser Leu Thr Ala Asp Ala Leu Gln Gln Ile Ser Asp Lys Tyr Asp
 100 105 110
 Gly Val Val Ala Glu Asn Lys Leu Leu Phe Leu Gln Arg Gln Tyr Tyr
 115 120 125
 Val Asp Asp Glu Gly Asn Val Arg Asp Gly Arg Asn Asn Asp Lys Ile
 130 135 140

Tyr Cys Glu Pro Lys His Val Tyr Asp Met Val Met Ala Thr His Leu
 145 150 155 160
 Met Asn Lys His Leu Arg Gly Lys Thr Leu His Ser Phe Leu Phe Ser
 165 170 175
 His Phe Ala Asn Ile Ser His Ala Ile Ile Asp Trp Val Gln Gln Phe
 180 185 190
 Cys Ser Lys Cys Asn Lys Lys Gly Lys Ile Lys Pro Leu Lys Glu Tyr
 195 200 205
 Lys Arg Pro Asp Met Tyr Asp Lys Leu Leu Pro Met Glu Arg Ile His
 210 215 220
 Ile Glu Val Phe Glu Pro Phe Asn Gly Glu Ala Ile Glu Gly Lys Tyr
 225 230 235 240
 Ser Tyr Val Leu Leu Cys Arg Asp Tyr Arg Ser Ser Phe Met Trp Leu
 245 250 255
 Leu Pro Leu Lys Ser Thr Lys Phe Lys His Leu Ile Pro Val Val Ser
 260 265 270
 Ser Leu Phe Leu Thr Phe Ala Arg Val Pro Ile Phe Val Thr Ser Ser
 275 280 285
 Thr Leu Asp Lys Asp Asp Leu Tyr Asp Ile Cys Glu Glu Ile Ala Ser
 290 295 300
 Lys Tyr Gly Leu Arg Ile Gly Leu Gly Leu Lys Ser Ser Ala Arg Phe
 305 310 315 320
 His Thr Gly Gly Ile Leu Cys Ile Gln Tyr Ala Leu Asn Ser Tyr Lys
 325 330 335
 Lys Glu Cys Leu Ala Asp Trp Gly Lys Cys Leu Arg Tyr Gly Pro Tyr
 340 345 350
 Arg Phe Asn Arg Arg Arg Asn Lys Arg Thr Lys Arg Lys Pro Val Gln
 355 360 365
 Val Leu Leu Ser Glu Val Pro Gly His Asn Ala Lys Phe Glu Thr Lys
 370 375 380
 Arg Glu Arg Val Ile Glu Asn Thr Tyr Ser Arg Asn Met Phe Lys Met
 385 390 395 400
 Ala Gly Gly Lys Gly Leu Ile Tyr Leu Glu Asp Val Asn Thr Phe Ala
 405 410 415
 Leu Ala Asn Glu Ala Asp Asn Ser Cys Asn Asn Asn Gly Ile Leu His
 420 425 430
 Asn Asn Asn Ile Gly Asn Asp Asn Phe Glu Glu Glu Val Gln Lys Gln
 435 440 445

Phe Asp Leu Thr Glu Lys Asn Tyr Ile Asp Glu Tyr Asp Asp Leu Ala
 450 455 460

His Asp Ser Ser Glu Gly Glu Phe Glu Pro Asn Thr Leu Thr Pro Glu
 465 470 475 480

Glu Lys Pro Pro His Asn Val Asp Glu Asp Arg Ile Glu Ser Thr Gly
 485 490 495

Val Ala Ala Pro Met Gln Gly Thr Glu Glu Pro Glu Lys Gly Asp Gln
 500 505 510

Lys Glu Ser Asp Gly Ala Ser Gln Val Asp Gln Ser Val Glu Ile Thr
 515 520 525

Arg Pro Glu Thr Ser Tyr Tyr Gln Thr Leu Glu Ser Pro Ser Thr Lys
 530 535 540

Arg Gln Lys Leu Asp Gln Gln Gly Asn Gly Asp Gln Thr Arg Asp Phe
 545 550 555 560

Gly Thr Ser Met Glu Leu
 565

<210> 26

<211> 309

<212> PRT

<213> Escherichia coli

<400> 26

Met Ala Arg Tyr Asp Leu Val Asp Arg Leu Asn Thr Thr Phe Arg Gln
 1 5 10 15

Met Glu Gln Glu Leu Ala Ile Phe Ala Ala His Leu Glu Gln His Lys
 20 25 30

Leu Leu Val Ala Arg Val Phe Ser Leu Pro Glu Val Lys Lys Glu Asp
 35 40 45

Glu His Asn Pro Leu Asn Arg Ile Glu Val Lys Gln His Leu Gly Asn
 50 55 60

Asp Ala Gln Ser Leu Ala Leu Arg His Phe Arg His Leu Phe Ile Gln
 65 70 75 80

Gln Gln Ser Glu Asn Arg Ser Ser Lys Ala Ala Val Arg Leu Pro Gly
 85 90 95

Val Leu Cys Tyr Gln Val Asp Asn Leu Ser Gln Ala Ala Leu Val Ser
 100 105 110

His Ile Gln His Ile Asn Lys Leu Lys Thr Thr Phe Glu His Ile Val
 115 120 125

Thr Val Glu Ser Glu Leu Pro Thr Ala Ala Arg Phe Glu Trp Val His
 130 135 140

Arg His Leu Pro Gly Leu Ile Thr Leu Asn Ala Tyr Arg Thr Leu Thr
 145 150 155 160
 Val Leu His Asp Pro Ala Thr Leu Arg Phe Gly Trp Ala Asn Lys His
 165 170 175
 Ile Ile Lys Asn Leu His Arg Asp Glu Val Leu Ala Gln Leu Glu Lys
 180 185 190
 Ser Leu Lys Ser Pro Arg Ser Val Ala Pro Trp Thr Arg Glu Glu Trp
 195 200 205
 Gln Arg Lys Leu Glu Arg Glu Tyr Gln Asp Ile Ala Ala Leu Pro Gln
 210 215 220
 Asn Ala Lys Leu Lys Ile Lys Arg Pro Val Lys Val Gln Pro Ile Ala
 225 230 235 240
 Arg Val Trp Tyr Lys Gly Asp Gln Lys Gln Val Gln His Ala Cys Pro
 245 250 255
 Thr Pro Leu Ile Ala Leu Ile Asn Arg Asp Asn Gly Ala Gly Val Pro
 260 265 270
 Asp Val Gly Glu Leu Leu Asn Tyr Asp Ala Asp Asn Val Gln His Arg
 275 280 285
 Tyr Lys Pro Gln Ala Gln Pro Leu Arg Leu Ile Ile Pro Arg Leu His
 290 295 300
 Leu Tyr Val Ala Asp
 305

<210> 27
 <211> 1698
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1698)

<400> 27
 atg acg aaa ccg cgt tac aat gac gtg ttg ttt gat gat gat gac tcg 48
 Met Thr Lys Pro Arg Tyr Asn Asp Val Leu Phe Asp Asp Asp Asp Ser
 1 5 10 15
 gta cca tca gaa tca gtt acg agg aaa tcg cag aga aga aag gca acg 96
 Val Pro Ser Glu Ser Val Thr Arg Lys Ser Gln Arg Arg Lys Ala Thr
 20 25 30
 tca cct ggg gaa tca aga gag tcc tca aaa gat cgt cta ctg ata ctt 144
 Ser Pro Gly Glu Ser Arg Glu Ser Ser Lys Asp Arg Leu Leu Ile Leu
 35 40 45

ccc tct atg ggg gaa tca tat act gag tac gta gac tct tat ttg aac	192
Pro Ser Met Gly Glu Ser Tyr Thr Glu Tyr Val Asp Ser Tyr Leu Asn	
50 55 60	
tta gaa tta ttg gaa agg gga gaa aga gaa aca cca atc ttt ctt gaa	240
Leu Glu Leu Leu Glu Arg Gly Glu Arg Glu Thr Pro Ile Phe Leu Glu	
65 70 75 80	
tct ctg aca aga caa cta acg cag aaa ata tat gaa cta ata aaa aca	288
Ser Leu Thr Arg Gln Leu Thr Gln Lys Ile Tyr Glu Leu Ile Lys Thr	
85 90 95	
aaa tct tta act gca gat gcc ttg caa caa ata agt gat aaa tac gat	336
Lys Ser Leu Thr Ala Asp Ala Leu Gln Gln Ile Ser Asp Lys Tyr Asp	
100 105 110	
ggg gta gtg gca gaa aac aag ctg tta ttt ttg caa aga cag tat tat	384
Gly Val Val Ala Glu Asn Lys Leu Leu Phe Leu Gln Arg Gln Tyr Tyr	
115 120 125	
gtt gat gat gaa gga aat gtt aga gat ggc cga aat aat gat aaa ata	432
Val Asp Asp Glu Gly Asn Val Arg Asp Gly Arg Asn Asn Asp Lys Ile	
130 135 140	
tac tgt gag cca aag cat gta tac gac atg gtg atg gca aca cac ttg	480
Tyr Cys Glu Pro Lys His Val Tyr Asp Met Val Met Ala Thr His Leu	
145 150 155 160	
atg aat aag cat ctt agg ggt aaa aca tta cat tcc ttt tta ttt tct	528
Met Asn Lys His Leu Arg Gly Lys Thr Leu His Ser Phe Leu Phe Ser	
165 170 175	
cat ttt gcc aat att agt cat gcc atc atc gat tgg gtc cag caa ttt	576
His Phe Ala Asn Ile Ser His Ala Ile Ile Asp Trp Val Gln Gln Phe	
180 185 190	
tgt tca aaa tgt aat aaa aag ggc aaa att aaa cca ttg aag gaa tat	624
Cys Ser Lys Cys Asn Lys Lys Gly Lys Ile Lys Pro Leu Lys Glu Tyr	
195 200 205	
aaa cgt cct gac atg tac gat aaa cta cta cca atg gaa agg ata cat	672
Lys Arg Pro Asp Met Tyr Asp Lys Leu Leu Pro Met Glu Arg Ile His	
210 215 220	
att gag gta ttc gaa ccc ttc aat gga gaa gct att gag gga aaa tat	720
Ile Glu Val Phe Glu Pro Phe Asn Gly Glu Ala Ile Glu Gly Lys Tyr	
225 230 235 240	
tct tat gtc ctt tta tgc cga gac tat cgc tct agt ttt atg tgg tta	768
Ser Tyr Val Leu Leu Cys Arg Asp Tyr Arg Ser Ser Phe Met Trp Leu	
245 250 255	
tta cca ctt aag agt acc aaa ttc aaa cat ctt atc cca gtt gtt tcc	816
Leu Pro Leu Lys Ser Thr Lys Phe Lys His Leu Ile Pro Val Val Ser	
260 265 270	

tca ctt ttt tta aca ttt gct agg gtt cca att ttc gta aca tca agc	864
Ser Leu Phe Leu Thr Phe Ala Arg Val Pro Ile Phe Val Thr Ser Ser	
275 280 285	
act tta gat aaa gat gat ctt tat gat att tgt gaa gaa att gca tca	912
Thr Leu Asp Lys Asp Asp Leu Tyr Asp Ile Cys Glu Glu Ile Ala Ser	
290 295 300	
aaa tac ggt ctc cgt att ggc ttg ggt ttg aag agt tct gcg aga ttt	960
Lys Tyr Gly Leu Arg Ile Gly Leu Gly Leu Lys Ser Ser Ala Arg Phe	
305 310 315 320	
cat act ggg ggt ata ctg tgc att cag tat gct cta aat agt tat aag	1008
His Thr Gly Gly Ile Leu Cys Ile Gln Tyr Ala Leu Asn Ser Tyr Lys	
325 330 335	
aag gaa tgt cta gcc gat tgg ggt aag tgc cta aga tat ggc cct tac	1056
Lys Glu Cys Leu Ala Asp Trp Gly Lys Cys Leu Arg Tyr Gly Pro Tyr	
340 345 350	
aga ttc aac cga agg aga aat aag aga acg aaa cgt aaa cct gtg caa	1104
Arg Phe Asn Arg Arg Arg Asn Lys Arg Thr Lys Arg Lys Pro Val Gln	
355 360 365	
gta cta ctt agt gaa gtt cca ggt cac aat gcc aag ttt gag act aag	1152
Val Leu Leu Ser Glu Val Pro Gly His Asn Ala Lys Phe Glu Thr Lys	
370 375 380	
aga gaa agg gtt ata gaa aac aca tat tcc cgt aat atg ttc aag atg	1200
Arg Glu Arg Val Ile Glu Asn Thr Tyr Ser Arg Asn Met Phe Lys Met	
385 390 395 400	
gca ggt gga aaa ggt ctt ata tat ttg gaa gat gtc aat act ttt gcc	1248
Ala Gly Gly Lys Gly Leu Ile Tyr Leu Glu Asp Val Asn Thr Phe Ala	
405 410 415	
ctt gct aat gaa gcg gat aat agc tgt aac aat aat gga att ctt cat	1296
Leu Ala Asn Glu Ala Asp Asn Ser Cys Asn Asn Asn Gly Ile Leu His	
420 425 430	
aat aac aat ata gga aat gat aac ttt gaa gaa gaa gtg caa aaa caa	1344
Asn Asn Asn Ile Gly Asn Asp Asn Phe Glu Glu Glu Val Gln Lys Gln	
435 440 445	
ttt gat cta act gaa aaa aac tat atc gat gag tat gat gat ttg gca	1392
Phe Asp Leu Thr Glu Lys Asn Tyr Ile Asp Glu Tyr Asp Asp Leu Ala	
450 455 460	
cat gat tct tca gag ggc gaa ttt gaa cct aat acc tta act ccc gaa	1440
His Asp Ser Ser Glu Gly Glu Phe Glu Pro Asn Thr Leu Thr Pro Glu	
465 470 475 480	
gaa aag cct cct cat aat gtc gat gag gac cga ata gag tcc acc ggc	1488
Glu Lys Pro Pro His Asn Val Asp Glu Asp Arg Ile Glu Ser Thr Gly	
485 490 495	

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gtg gca gcc cca atg cag gga aca gaa gag cct gaa aaa ggg gat caa 1536
Val Ala Ala Pro Met Gln Gly Thr Glu Glu Pro Glu Lys Gly Asp Gln
      500                505                510

aaa gaa agt gac ggt gca tca caa gta gat caa agt gtc gaa ata act 1584
Lys Glu Ser Asp Gly Ala Ser Gln Val Asp Gln Ser Val Glu Ile Thr
      515                520                525

aga cca gaa act tcc tac tat caa act ctg gaa tcg ccg tca aca aaa 1632
Arg Pro Glu Thr Ser Tyr Tyr Gln Thr Leu Glu Ser Pro Ser Thr Lys
      530                535                540

cga cag aaa tta gac caa cag ggt aat gga gat caa aca aga gac ttt 1680
Arg Gln Lys Leu Asp Gln Gln Gly Asn Gly Asp Gln Thr Arg Asp Phe
      545                550                555                560

ggc aca tca atg gaa ttg 1698
Gly Thr Ser Met Glu Leu
      565

<210> 28
<211> 927
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1) .. (927)

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Met Ala Arg Tyr Asp Leu Val Asp Arg Leu Asn Thr Thr Phe Arg Gln
      1                5                10                15

atg gaa caa gag ctg gct ata ttt gcc gct cat ctt gag caa cac aag 96
Met Glu Gln Glu Leu Ala Ile Phe Ala Ala His Leu Glu Gln His Lys
      20                25                30

cta ttg gtt gcc cgc gtg ttc tct ttg ccg gag gta aaa aaa gag gat 144
Leu Leu Val Ala Arg Val Phe Ser Leu Pro Glu Val Lys Lys Glu Asp
      35                40                45

gag cat aat ccg ctt aat cgt att gag gta aaa caa cat ctc ggc aac 192
Glu His Asn Pro Leu Asn Arg Ile Glu Val Lys Gln His Leu Gly Asn
      50                55                60

gac gcg cag tcg ctg gcg ttg cgt cat ttc cgc cat tta ttt att caa 240
Asp Ala Gln Ser Leu Ala Leu Arg His Phe Arg His Leu Phe Ile Gln
      65                70                75                80

caa cag tcc gaa aat cgc agc agc aag gcc gct gtc cgt ctg cct ggc 288
Gln Gln Ser Glu Asn Arg Ser Ser Lys Ala Ala Val Arg Leu Pro Gly
      85                90                95

gtg ttg tgt tac cag gtc gat aac ctt tcg caa gca gcg ttg gtc agt 336
Val Leu Cys Tyr Gln Val Asp Asn Leu Ser Gln Ala Ala Leu Val Ser
      100                105                110

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cat att cag cac atc aat aaa ctc aag acc acg ttc gag cat atc gtc	384
His Ile Gln His Ile Asn Lys Leu Lys Thr Thr Phe Glu His Ile Val	
115 120 125	
acg gtt gaa tca gaa ctc ccc acc gcg gca cgt ttt gaa tgg gtg cat	432
Thr Val Glu Ser Glu Leu Pro Thr Ala Ala Arg Phe Glu Trp Val His	
130 135 140	
cgt cat ttg ccg ggg ctg atc acc ctt aat gct tac cgc acg ctc acc	480
Arg His Leu Pro Gly Leu Ile Thr Leu Asn Ala Tyr Arg Thr Leu Thr	
145 150 155 160	
gtt ctg cac gac ccc gcc act tta cgc ttt ggt tgg gct aat aaa cat	528
Val Leu His Asp Pro Ala Thr Leu Arg Phe Gly Trp Ala Asn Lys His	
165 170 175	
atc att aag aat tta cat cgt gat gaa gtc ctg gca cag ctg gaa aaa	576
Ile Ile Lys Asn Leu His Arg Asp Glu Val Leu Ala Gln Leu Glu Lys	
180 185 190	
agc ctg aaa tca cca cgc agt gtc gca ccg tgg acg cgc gag gag tgg	624
Ser Leu Lys Ser Pro Arg Ser Val Ala Pro Trp Thr Arg Glu Glu Trp	
195 200 205	
caa aga aaa ctg gag cga gag tat cag gat atc gct gcc ctg cca cag	672
Gln Arg Lys Leu Glu Arg Glu Tyr Gln Asp Ile Ala Ala Leu Pro Gln	
210 215 220	
aac gcg aag tta aaa atc aaa cgt ccg gtg aag gtg cag ccg att gcc	720
Asn Ala Lys Leu Lys Ile Lys Arg Pro Val Lys Val Gln Pro Ile Ala	
225 230 235 240	
cgc gtc tgg tac aaa gga gat caa aaa caa gtc caa cac gcc tgc cct	768
Arg Val Trp Tyr Lys Gly Asp Gln Lys Gln Val Gln His Ala Cys Pro	
245 250 255	
aca cca ctg att gca ctg att aat cgg gat aat ggc gcg ggc gtg ccg	816
Thr Pro Leu Ile Ala Leu Ile Asn Arg Asp Asn Gly Ala Gly Val Pro	
260 265 270	
gac gtt ggt gag ttg tta aat tac gat gcc gac aat gtg cag cac cgt	864
Asp Val Gly Glu Leu Leu Asn Tyr Asp Ala Asp Asn Val Gln His Arg	
275 280 285	
tat aaa cct cag gcg cag ccg ctt cgt ttg atc att cca cgg ctg cac	912
Tyr Lys Pro Gln Ala Gln Pro Leu Arg Leu Ile Ile Pro Arg Leu His	
290 295 300	
ctg tat gtt gca gat	927
Leu Tyr Val Ala Asp	
305	